

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/586,978
Source: IFWP
Date Processed by STIC: 08/03/2006

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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/586,978

DATE: 08/03/2006

TIME: 09:46:39

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Output Set: N:\CRF4\08032006\J586978.raw

3 <110> APPLICANT: Kohonen-Corish, Maija
 5 <120> TITLE OF INVENTION: Methods of diagnosing colorectal cancer and reagents
 therefor
 7 <130> FILE REFERENCE: RICE-029
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/586,978
 C--> 9 <141> CURRENT FILING DATE: 2006-07-20
 9 <150> PRIOR APPLICATION NUMBER: AU 2004900340
 10 <151> PRIOR FILING DATE: 2004-01-23
 12 <150> PRIOR APPLICATION NUMBER: US 60/540,662
 13 <151> PRIOR FILING DATE: 2004-01-29
 15 <150> PRIOR APPLICATION NUMBER: PCT/AU2005/000077
 16 <151> PRIOR FILING DATE: 2005-01-24
 18 <160> NUMBER OF SEQ ID NOS: 46
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 4181
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (221)..(2707)
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 37 tgtggcagaa gggaccaaggc agtggatatt gagcctgtga agtccaaactc ttaagctccg 180
 39 agacctgggg gactgagagc ccagctctga aaagtgcatac atg aat tcc gga gtt 235
 40 Met Asn Ser Gly Val
 41 1 5
 43 gcc atg aaa tat gga aac gac tcc tcg gcc gag ctg agt gag ctc cat 283
 44 Ala Met Lys Tyr Gly Asn Asp Ser Ser Ala Glu Leu Ser Glu Leu His
 45 10 15 20
 47 tca gca gcc ctg gca tca cta aag gga gat ata gtg gaa ctt aat aaa 331
 48 Ser Ala Ala Leu Ala Ser Leu Lys Gly Asp Ile Val Glu Leu Asn Lys
 49 25 30 35
 51 cgt ctc cag caa aca gag agg gaa cgg gac ctt ctg gaa aag aaa ttg 379
 52 Arg Leu Gln Gln Thr Glu Arg Glu Arg Asp Leu Leu Glu Lys Lys Leu
 53 40 45 50
 55 gcc aag gca cag tgc gag cag tcc cac ctc atg aga gag cat gag gat 427
 56 Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met Arg Glu His Glu Asp
 57 55 60 65
 59 gtc cag gag cga acg acg ctt cgc tat gag gaa cgc atc aca gag ctc 475
 60 Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu Arg Ile Thr Glu Leu
 61 70 75 80 85
 63 cac agc gtc att gcg gag ctc aac aag aag ata gac cgt ctg caa ggc 523

(Pg-6)

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65				90					95					100			
67	acc	acc	atc	agg	gag	gaa	gat	gag	tac	tca	gaa	ctg	cga	tca	gaa	ctc	571
68	Thr	Thr	Ile	Arg	Glu	Glu	Asp	Glu	Tyr	Ser	Glu	Leu	Arg	Ser	Glu	Leu	
69				105					110				115				
71	agc	cag	agc	caa	cac	gag	gtc	aac	gag	gac	tct	cga	agc	atg	gac	caa	619
72	Ser	Gln	Ser	Gln	His	Glu	Val	Asn	Glu	Asp	Ser	Arg	Ser	Met	Asp	Gln	
73					120				125			130					
75	gac	cag	acc	tct	tct	atc	ccc	gaa	aac	cag	tct	acc	atg	gtt	act	667	
76	Asp	Gln	Thr	Ser	Val	Ser	Ile	Pro	Glu	Asn	Gln	Ser	Thr	Met	Val	Thr	
77					135				140			145					
79	gct	gac	atg	gac	aac	tgc	agt	gac	ctg	aac	tca	gaa	ctg	cag	agg	gtg	715
80	Ala	Asp	Met	Asp	Asn	Cys	Ser	Asp	Leu	Asn	Ser	Glu	Leu	Gln	Arg	Val	
81	150				155				160			165					
83	ctg	aca	ggg	ctg	gag	aat	gtt	gtc	tgc	ggc	agg	aag	aag	agc	agc	tgc	763
84	Leu	Thr	Gly	Leu	Glu	Asn	Val	Val	Cys	Gly	Arg	Lys	Lys	Ser	Ser	Cys	
85					170				175			180					
87	agc	ctc	tcc	gtg	gcc	gag	gtg	gac	agg	cac	att	gag	cag	ctc	acc	aca	811
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89					185				190			195					
91	gcc	agc	gag	cac	tgt	gac	ctg	gct	att	aag	aca	gtc	gag	gag	att	gag	859
92	Ala	Ser	Glu	His	Cys	Asp	Leu	Ala	Ile	Lys	Thr	Val	Glu	Glu	Ile	Glu	
93					200				205			210					
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99	cgg	tgg	gag	aag	gag	ctg	gct	ggg	ctg	agg	gaa	gag	aat	gag	agc	ctg	955
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104	Thr	Ala	Met	Leu	Cys	Ser	Lys	Glu	Glu	Glu	Leu	Asn	Arg	Thr	Lys	Ala	
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112	Arg	Glu	Leu	Gln	Thr	Arg	Leu	Gln	Ser	Val	Gln	Ala	Thr	Gly	Pro	Ser	
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115	agc	cct	ggc	cgc	ctc	act	tcc	acc	aac	cg	cg	att	aa	ccc	agc	act	1147
116	Ser	Pro	Gly	Arg	Leu	Thr	Ser	Thr	Asn	Arg	Pro	Ile	Asn	Pro	Ser	Thr	
117					295				300			305					
119	ggg	gag	ctg	agc	aca	agc	agc	agc	aat	gac	att	ccc	atc	gcc	aag	1195	
120	Gly	Glu	Leu	Ser	Thr	Ser	Ser	Ser	Asn	Asp	Ile	Pro	Ile	Ala	Lys		
121	310				315				320			325					
123	att	gct	gag	agg	gt	aag	cta	tca	aag	aca	agg	tcc	gaa	tcg	tca	tca	1243
124	Ile	Ala	Glu	Arg	Val	Lys	Leu	Ser	Lys	Thr	Arg	Ser	Glu	Ser	Ser	Ser	
125					330				335			340					
127	tct	gat	cg	cca	gtc	ctg	ggc	tca	gaa	atc	agt	agc	ata	ggg	gta	tcc	1291
128	Ser	Asp	Arg	Pro	Val	Leu	Gly	Ser	Glu	Ile	Ser	Ser	Ile	Gly	Val	Ser	

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132	Ser Ser Val Ala Glu His Leu Ala His Ser Leu Gln Asp Cys Ser Asn			
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135	atc caa gag att ttc caa aca ctc tac tca cac gga tct gcc atc tca			1387
136	Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His Gly Ser Ala Ile Ser			
137	375	380	385	
139	gaa agc aag att aga gag ttt gag gtg gaa aca gaa cgg ctg aat agc			1435
140	Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr Glu Arg Leu Asn Ser			
141	390	395	400	405
143	cgg att gag cac ctc aaa tcc caa aat gac ctc ctg acc ata acc ttg			1483
144	Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu Leu Thr Ile Thr Leu			
145	410	415	420	
147	gag gaa tgt aaa agc aat gct gag agg atg agc atg ctg gtg gga aaa			1531
148	Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser Met Leu Val Gly Lys			
149	425	430	435	
151	tac gaa tcc aat gcc aca gcg ctg agg ctg gcc ttg cag tac agc gag			1579
152	Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala Leu Gln Tyr Ser Glu			
153	440	445	450	
155	cag tgc atc gaa gcc tac gaa ctc ctc ctg gca gag agt gag			1627
156	Gln Cys Ile Glu Ala Tyr Glu Leu Leu Ala Leu Ala Glu Ser Glu			
157	455	460	465	
159	cag agc ctc atc ctg ggg cag ttc cga gcg ggc gtg ggg tcc tcc			1675
160	Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala Gly Val Gly Ser Ser			
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163	cct gga gac cag tcg ggg gat gaa aac atc act cag atg ctc aag cga			1723
164	Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr Gln Met Leu Lys Arg			
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172	Met Lys Leu Asp Gly Ser Cys Gly Ala Phe Ala Val Ala Gly Cys			
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179	acc agc tcc aca gcc agt agt tgc gac acc gag ttc act aaa gaa gac			1915
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183	gag cag agg ctg aag gat tat atc cag cag ctc aag aat gac agg gct			1963
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187	gcg gtc aag ctg acc atg ctg gag ctg gaa agc atc cac atc gat cct			2011
188	Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser Ile His Ile Asp Pro			
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192	Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser Gln Arg Leu Asp Leu			
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200 Ala Glu Leu Lys Ala Gln Leu Tyr Leu Leu Glu Lys Glu Lys Lys Ala	
201 630 635 640 645	
203 ctg gag ctg aag ctg agc acg cgg gag gcc cag gag cag gcc tac ctg	2203
204 Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln Glu Gln Ala Tyr Leu	
205 650 655 660	
207 gtg cac att gag cac ctg aag tcc gag gtg gag gag cag aag gag cag	2251
208 Val His Ile Glu His Leu Lys Ser Glu Val Glu Glu Gln Lys Glu Gln	
209 665 670 675	
211 cgg atg cga tcc ctc agc tcc acc agc agc ggc agc aaa gat aaa cct	2299
212 Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly Ser Lys Asp Lys Pro	
213 680 685 690	
215 ggc aag gag tgt gat gct gct gcc tcc cca gct ctg tcc cta gct gaa	2347
216 Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala Leu Ser Leu Ala Glu	
217 695 700 705	
219 ctc agg aca acg tgc agc gag aat gag ctg gct gcg gag ttc acc aac	2395
220 Leu Arg Thr Thr Cys Ser Glu Asn Glu Leu Ala Ala Glu Phe Thr Asn	
221 710 715 720 725	
223 gcc att cgt cga gaa aag aag ttg aag gcc aga gtt caa gag ctg gtg	2443
224 Ala Ile Arg Arg Glu Lys Lys Leu Lys Ala Arg Val Gln Glu Leu Val	
225 730 735 740	
227 agt gcc ttg gag aga ctc acc aag agc agt gaa atc cga cat cag caa	2491
228 Ser Ala Leu Glu Arg Leu Thr Lys Ser Ser Glu Ile Arg His Gln Gln	
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232 Ser Ala Glu Phe Val Asn Asp Leu Lys Arg Ala Asn Ser Asn Leu Val	
233 760 765 770	
235 gct gcc tat gag aaa gca aag aaa aag cat caa aac aaa ctg aag aag	2587
236 Ala Ala Tyr Glu Lys Ala Lys Lys His Gln Asn Lys Leu Lys Lys	
237 775 780 785	
239 tta gag tcg cag atg atg gcc atg gtg gag aga cat gag acc caa gtg	2635
240 Leu Glu Ser Gln Met Met Ala Met Val Glu Arg His Glu Thr Gln Val	
241 790 795 800 805	
243 agg atg ctc aag caa aga ata gct ctg cta gag gag gag aac tcc agg	2683
244 Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu Glu Glu Asn Ser Arg	
245 810 815 820	
247 cca cac acc aat gaa act tcg ctt taatcagcac tcacgcaccc gagttctgcc	2737
248 Pro His Thr Asn Glu Thr Ser Leu	
249 825	
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255 aacccttggg gtgactggcc atggtagat tggactgt atccagaggt gcccgtctt	2917
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279	ctcccgccc	cagggacta	cataattgt	gttctgctga	atcaaatctc	ttccacatgg	3637									
281	gtgcatttgc	agctctggac	ctgtctctac	ctaaggacaa	gacactgagg	agatactgaa	3697									
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295	tgaaaaatgt	gttccattgc	catagctgac	tacaaattaa	agttgaggag	gtttctgcat	4117									
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 9521

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:9467